

SEQUENCE LISTING

<110> EISAI CO., LTD.

<120> Novel gene participating in epidermal differentiation and use thereof

<130> E1-A0208P

<150> 2004-03-02

<151> JP 2004-057559

<160> 53

<170> PatentIn version 3.1

<210> 1

<211> 661

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (23)..(337)

<223>

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Met Lys Pro Val Thr Ala Ser Ala Leu Leu

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ctt atc ctg ctg ggt gtg gcc tgg cgt gga gac agc cac agc tgg ggt 100

Leu Ile Leu Leu Gly Val Ala Trp Arg Gly Asp Ser His Ser Trp Gly

15

20

25

tca gat ctg tca tct ctg cag aag agg gca ggt gga gct gac cag ttt 148

Ser Asp Leu Ser Ser Leu Gln Lys Arg Ala Gly Gly Ala Asp Gln Phe

30

35

40

tct aag cct gaa gca aga caa gat ctt tca gct gac tca tcc aag aac 196
 Ser Lys Pro Glu Ala Arg Gln Asp Leu Ser Ala Asp Ser Ser Lys Asn
 45 50 55

tac tac aat aac cag cag gtg aat cct act tac aac tgg caa tac tat 244
 Tyr Tyr Asn Asn Gln Gln Val Asn Pro Thr Tyr Asn Trp Gln Tyr Tyr
 60 65 70

acc aag acc act gcc aag gcg gga gtc aca cct tca tct tcc tgg gct 292
 Thr Lys Thr Thr Ala Lys Ala Gly Val Thr Pro Ser Ser Ser Ser Ala
 75 80 85 90

tcc cgg gca caa cct ggc ctg ctg aag tgg ctg aag ttt tgg tag 337
 Ser Arg Ala Gln Pro Gly Leu Leu Lys Trp Leu Lys Phe Trp
 95 100

aacattcctt ctagtcactg cggactcctc acgaatgcac acaggtcttc agggagtttg 397

actgtcctta cccagagtcc tctctgatgc agctgacctc cctgggcatg acaagcctgt 457

catctcgctt ggggacctgg tttatctgtc ctcatctctc ccattcgatt gtggtgtctt 517

ggcgactaat cagtttcatt gtataaccag ccagatcttc acctcttctt ccgtacgtga 577

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<211> 104

<212> PRT

<213> Mus musculus

<400> 2

Met Lys Pro Val Thr Ala Ser Ala Leu Leu Leu Ile Leu Leu Gly Val

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Ala Trp Arg Gly Asp Ser His Ser Trp Gly Ser Asp Leu Ser Ser Leu			
20	25	30	
Gln Lys Arg Ala Gly Gly Ala Asp Gln Phe Ser Lys Pro Glu Ala Arg			
35	40	45	
Gln Asp Leu Ser Ala Asp Ser Ser Lys Asn Tyr Tyr Asn Asn Gln Gln			
50	55	60	
Val Asn Pro Thr Tyr Asn Trp Gln Tyr Tyr Thr Lys Thr Thr Ala Lys			
65	70	75	80
Ala Gly Val Thr Pro Ser Ser Ser Ser Ala Ser Arg Ala Gln Pro Gly			
85	90	95	
Leu Leu Lys Trp Leu Lys Phe Trp			
100			

<210> 3
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 <212> DNA
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<220>
 <221> CDS
 <222> (170)..(1723)
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 atagactggg ctgcagacat cctcagagga gagagggagc tgggcagag atg aag cta 178

Met Lys Leu

1

cag ggc tct ctg gcc tgc ctc ctg ctg gcc cta tgt ctg ggt ggt ggg	226
Gln Gly Ser Leu Ala Cys Leu Leu Leu Ala Leu Cys Leu Gly Gly Gly	
5 10 15	
 gca gct aac ccg ctg cac agt gga ggg gag ggc aca ggg gca agt gct	274
Ala Ala Asn Pro Leu His Ser Gly Gly Glu Gly Thr Gly Ala Ser Ala	
20 25 30 35	
 gcc cat gga gca gga gat gcc att agc cat gga att gga gag gct gtg	322
Ala His Gly Ala Gly Asp Ala Ile Ser His Gly Ile Gly Glu Ala Val	
40 45 50	
 ggc caa ggg gct aaa gaa gca gcc agc tct gga atc cag aat gcc cta	370
Gly Gln Gly Ala Lys Glu Ala Ala Ser Ser Gly Ile Gln Asn Ala Leu	
55 60 65	
 ggc cag ggg cac gga gag gaa ggt ggc tcc aca ttg atg ggg agc aga	418
Gly Gln Gly His Gly Glu Glu Gly Gly Ser Thr Leu Met Gly Ser Arg	
70 75 80	
 ggc gat gtt ttt gag cac cgg ctt ggg gaa gca gca aga tct ctg ggg	466
Gly Asp Val Phe Glu His Arg Leu Gly Glu Ala Ala Arg Ser Leu Gly	
85 90 95	
 aac gct ggg aat gag att ggc aga cag gct gag gat atc att cgc caa	514
Asn Ala Gly Asn Glu Ile Gly Arg Gln Ala Glu Asp Ile Ile Arg Gln	
100 105 110 115	
 ggg gta gat gct gtc cac aac gct ggg tcc tgg ggg aca tct gga ggt	562
Gly Val Asp Ala Val His Asn Ala Gly Ser Trp Gly Thr Ser Gly Gly	
120 125 130	
 cat ggc gca tat ggc tct caa ggt ggt gct gga gtc cag ggc aat cct	610
His Gly Ala Tyr Gly Ser Gln Gly Gly Ala Gly Val Gln Gly Asn Pro	

135	140	145	
ggt cct caa ggg aca ccc tgg gcc tca gga ggc aac tat ggg act aac			658
Gly Pro Gln Gly Thr Pro Trp Ala Ser Gly Gly Asn Tyr Gly Thr Asn			
150	155	160	
tct ctg ggt ggc tct gtg ggt cag ggt ggc aat ggc gga cca ctc aac			706
Ser Leu Gly Gly Ser Val Gly Gln Gly Gly Asn Gly Gly Pro Leu Asn			
165	170	175	
tat gaa acc aat gcc cag gga gct gtg gct cag cct ggc tac ggg aca			754
Tyr Glu Thr Asn Ala Gln Gly Ala Val Ala Gln Pro Gly Tyr Gly Thr			
180	185	190	195
gtg aga ggc aac aac cag aac tca ggg tgt acc aac ccc cca cct tct			802
Val Arg Gly Asn Asn Gln Asn Ser Gly Cys Thr Asn Pro Pro Pro Ser			
200	205	210	
ggc tcc cat gaa agc ttc agt aac tct ggg gga agc agc aat gat ggc			850
Gly Ser His Glu Ser Phe Ser Asn Ser Gly Gly Ser Ser Asn Asp Gly			
215	220	225	
agt cgt ggt agc caa ggc agt cat ggc agt aat ggt cag ggc agc agc			898
Ser Arg Gly Ser Gln Gly Ser His Gly Ser Asn Gly Gln Gly Ser Ser			
230	235	240	
ggt aga ggc ggt ggc caa ggc aac agc gac aac aat ggc agc agt agc			946
Gly Arg Gly Gly Gly Gln Gly Asn Ser Asp Asn Asn Gly Ser Ser Ser			
245	250	255	
agt agc agc ggc agc aac agt ggc aac agc aac agt ggc aac agc ggc			994
Ser Ser Ser Gly Ser Asn Ser Gly Asn Ser Asn Ser Gly Asn Ser Gly			
260	265	270	275
aac agc aac agt ggc aac agc ggc aac agc ggt tct ggg tcc cgg gac			1042
Asn Ser Asn Ser Gly Asn Ser Gly Asn Ser Gly Ser Gly Ser Arg Asp			
280	285	290	

ata gaa aca tct aat ttt gat gaa ggc tat tcg gtc tcc agg gga acc	1090
Ile Glu Thr Ser Asn Phe Asp Glu Gly Tyr Ser Val Ser Arg Gly Thr	
295 300 305	
ggc agc agg ggt gga agt ggt gga agt ggt gga agt ggt gga agt ggt	1138
Gly Ser Arg Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly	
310 315 320	
gga agt ggt gga agt ggt ggt gga aac aaa ccc gag tgt aac aac cca	1186
Gly Ser Gly Gly Ser Gly Gly Gly Asn Lys Pro Glu Cys Asn Asn Pro	
325 330 335	
ggg aat gat gtg cgc atg gcc gga gga tct ggg agt cag ggg cat ggg	1234
Gly Asn Asp Val Arg Met Ala Gly Gly Ser Gly Ser Gln Gly His Gly	
340 345 350 355	
tcc aat ggt ggc aat ata caa aaa gaa gct gtc aat gga ctc aac act	1282
Ser Asn Gly Gly Asn Ile Gln Lys Glu Ala Val Asn Gly Leu Asn Thr	
360 365 370	
atg aac tcg gat gca tct acc ttg ccc ttc aac att gac aat ttc tgg	1330
Met Asn Ser Asp Ala Ser Thr Leu Pro Phe Asn Ile Asp Asn Phe Trp	
375 380 385	
gag aat ctt aag tcc aag acg cgc ttc att aac tgg gat gcc ata aac	1378
Glu Asn Leu Lys Ser Lys Thr Arg Phe Ile Asn Trp Asp Ala Ile Asn	
390 395 400	
aag ggt cat gcc cca tct ccc agc act cgg gct tta ctc tac ttc cgc	1426
Lys Gly His Ala Pro Ser Pro Ser Thr Arg Ala Leu Leu Tyr Phe Arg	
405 410 415	
aaa ctg tgg gag aat ttc aaa cgc agc act cct ttc ttc aac tgg aaa	1474
Lys Leu Trp Glu Asn Phe Lys Arg Ser Thr Pro Phe Phe Asn Trp Lys	
420 425 430 435	

cag att gag ggt tca gat ctg tca tct ctg cag aag agg gca ggt gga	1522
Gln Ile Glu Gly Ser Asp Leu Ser Ser Leu Gln Lys Arg Ala Gly Gly	
440 445 450	
 gct gac cag ttt tct aag cct gaa gca aga caa gat ctt tca gct gac	1570
Ala Asp Gln Phe Ser Lys Pro Glu Ala Arg Gln Asp Leu Ser Ala Asp	
455 460 465	
 tca tcc aag aac tac tac aat aac cag cag gtg aat cct act tac aac,	1618
Ser Ser Lys Asn Tyr Tyr Asn Asn Gln Gln Val Asn Pro Thr Tyr Asn	
470 475 480	
 tgg caa tac tat acc aag acc act gcc aag gcg gga gtc aca cct tca	1666
Trp Gln Tyr Tyr Thr Lys Thr Thr Ala Lys Ala Gly Val Thr Pro Ser	
485 490 495	
 tct tcc tgg gct tcc cgg gca caa cct ggc ctg ctg aag tgg ctg aag	1714
Ser Ser Ser Ala Ser Arg Ala Gln Pro Gly Leu Leu Lys Trp Leu Lys	
500 505 510 515	
 ttt tgg tag aacattcctt ctagtcactg cggactcctc acgaatgcac	1763
Phe Trp	
 acaggctcttc agggagtttg actgtcctta cccagagtcc tctctgatgc agctgaccta	1823
cctgggcatg acaagcctgt catctcgccct ggggacctgg tttatctgtc ctcatctccc	1883
ccattcgatt gtggtgtctt ggcgactaat cagtttcatt gtataaccag ccagatcttc	1943
acctcttctt ccgtacgtga ccgcaagtcc ctggaacgag gcatctggag cttcctactc	2003
tccagtttct ctgtggaaat aaaacatgac tctttgtttc	2043

<210> 4

<211> 517

<212> PRT

<213> Mus musculus

<400> 4

Met Lys Leu Gln Gly Ser Leu Ala Cys Leu Leu Leu Ala Leu Cys Leu
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Gly Gly Gly Ala Ala Asn Pro Leu His Ser Gly Gly Glu Gly Thr Gly
 20 25 30

Ala Ser Ala Ala His Gly Ala Gly Asp Ala Ile Ser His Gly Ile Gly
 35 40 45

Glu Ala Val Gly Gln Gly Ala Lys Glu Ala Ala Ser Ser Gly Ile Gln
 50 55 60

Asn Ala Leu Gly Gln Gly His Gly Glu Glu Gly Gly Ser Thr Leu Met
 65 70 75 80

Gly Ser Arg Gly Asp Val Phe Glu His Arg Leu Gly Glu Ala Ala Arg
 85 90 95

Ser Leu Gly Asn Ala Gly Asn Glu Ile Gly Arg Gln Ala Glu Asp Ile
 100 105 110

Ile Arg Gln Gly Val Asp Ala Val His Asn Ala Gly Ser Trp Gly Thr
 115 120 125

Ser Gly Gly His Gly Ala Tyr Gly Ser Gln Gly Gly Ala Gly Val Gln
 130 135 140

Gly Asn Pro Gly Pro Gln Gly Thr Pro Trp Ala Ser Gly Gly Asn Tyr
 145 150 155 160

Gly Thr Asn Ser Leu Gly Gly Ser Val Gly Gln Gly Gly Asn Gly Gly
 165 170 175

Pro Leu Asn Tyr Glu Thr Asn Ala Gln Gly Ala Val Ala Gln Pro Gly
 180 185 190

Tyr Gly Thr Val Arg Gly Asn Asn Gln Asn Ser Gly Cys Thr Asn Pro
 195 200 205

Pro Pro Ser Gly Ser His Glu Ser Phe Ser Asn Ser Gly Gly Ser Ser
 210 215 220

Asn Asp Gly Ser Arg Gly Ser Gln Gly Ser His Gly Ser Asn Gly Gln
 225 230 235 240

Gly Ser Ser Gly Arg Gly Gly Gly Gln Gly Asn Ser Asp Asn Asn Gly
 245 250 255

Ser Ser Ser Ser Ser Ser Gly Ser Asn Ser Gly Asn Ser Asn Ser Gly
 260 265 270

Asn Ser Gly Asn Ser Asn Ser Gly Asn Ser Gly Asn Ser Gly Ser Gly
 275 280 285

Ser Arg Asp Ile Glu Thr Ser Asn Phe Asp Glu Gly Tyr Ser Val Ser
 290 295 300

Arg Gly Thr Gly Ser Arg Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
 305 310 315 320

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly Asn Lys Pro Glu Cys
 325 330 335

Asn Asn Pro Gly Asn Asp Val Arg Met Ala Gly Gly Ser Gly Ser Gln
 340 345 350

Gly His Gly Ser Asn Gly Gly Asn Ile Gln Lys Glu Ala Val Asn Gly
 355 360 365

Leu Asn Thr Met Asn Ser Asp Ala Ser Thr Leu Pro Phe Asn Ile Asp

370	375	380
Asn Phe Trp Glu Asn Leu Lys Ser Lys Thr Arg Phe Ile Asn Trp Asp		
385	390	395 400
Ala Ile Asn Lys Gly His Ala Pro Ser Pro Ser Thr Arg Ala Leu Leu		
405	410	415
Tyr Phe Arg Lys Leu Trp Glu Asn Phe Lys Arg Ser Thr Pro Phe Phe		
420	425	430
Asn Trp Lys Gln Ile Glu Gly Ser Asp Leu Ser Ser Leu Gln Lys Arg		
435	440	445
Ala Gly Gly Ala Asp Gln Phe Ser Lys Pro Glu Ala Arg Gln Asp Leu		
450	455	460
Ser Ala Asp Ser Ser Lys Asn Tyr Tyr Asn Asn Gln Gln Val Asn Pro		
465	470	475 480
Thr Tyr Asn Trp Gln Tyr Tyr Thr Lys Thr Thr Ala Lys Ala Gly Val		
485	490	495
Thr Pro Ser Ser Ser Ser Ala Ser Arg Ala Gln Pro Gly Leu Leu Lys		
500	505	510
Trp Leu Lys Phe Trp		
515		

<210> 5
<211> 610
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (16).. (282)

<223>

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Met Lys Pro Ala Thr Ala Ser Ala Leu Leu Leu Leu

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ctg ctg ggc ctg gcc tgg acc cag ggg agc cac ggc tgg ggt gcg gac 99

Leu Leu Gly Leu Ala Trp Thr Gln Gly Ser His Gly Trp Gly Ala Asp

15

20

25

gcg tca tca ctg cag aaa cgt gca ggc aga gcc gat cag aac tac aat 147

Ala Ser Ser Leu Gln Lys Arg Ala Gly Arg Ala Asp Gln Asn Tyr Asn

30

35

40

tac aac cag cat gcg tat ccc act gcc tat ggt ggg aag tac tca gtc 195

Tyr Asn Gln His Ala Tyr Pro Thr Ala Tyr Gly Gly Lys Tyr Ser Val

45

50

55

60

aag acc cct gca aag ggg gga gtc tca cct tct tcc tcg gct tcc cgg 243

Lys Thr Pro Ala Lys Gly Gly Val Ser Pro Ser Ser Ser Ala Ser Arg

65

70

75

gtg caa cct ggc ctg ctg cag tgg gtg aag ttt tgg tag gcaatttctt 292

Val Gln Pro Gly Leu Leu Gln Trp Val Lys Phe Trp

80

85

gcaaccacca ccgaggcccc gaaaagcact ggtcgtcagg gagctcctcc ccttggtcccc 352

cagcctgtgc cagccctggc ccggctgcca cacctctgtt tcctaggctg gggaccacgc 412

ttgtctctcc ttgtttcttc ccactgcact gtggtgcttc agtggccacc agcctcgtca 472

catacaccag catctttctg tacctcctcc ctttggtgac ctgaagtcac tgtgacagtt 532

ctccaggaag gaggagcttc ctacttttga gtttctctgt ggaaataaaa catgaatctt 592

gtttccctaa aaaaaaaaa

610

<210> 6

<211> 88

<212> PRT

<213> Homo sapiens

<400> 6

Met Lys Pro Ala Thr Ala Ser Ala Leu Leu Leu Leu Leu Gly Leu
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Ala Trp Thr Gln Gly Ser His Gly Trp Gly Ala Asp Ala Ser Ser Leu
20 25 30

Gln Lys Arg Ala Gly Arg Ala Asp Gln Asn Tyr Asn Tyr Asn Gln His
35 40 45

Ala Tyr Pro Thr Ala Tyr Gly Gly Lys Tyr Ser Val Lys Thr Pro Ala
50 55 60

Lys Gly Gly Val Ser Pro Ser Ser Ser Ala Ser Arg Val Gln Pro Gly
65 70 75 80

Leu Leu Gln Trp Val Lys Phe Trp
85

<210> 7

<211> 1982

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (178)..(1608)

<223>

<400> 7

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ggacagggag tcggaaggag gaggacagag gagggcacag agacgcagag caagggcggc 120

aaggaggaga ccctggtggg aggaagacac tctggagaga gagggggctg ggcagag 177

atg aag ttc cag ggg ccc ctg gcc tgc ctc ctg ctg gcc ctc tgc ctg 225

Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys Leu

1 5 10 15

ggc agt ggg gag gct ggc ccc ctg cag agc gga gag gaa agc act ggg 273

Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser Thr Gly

20 25 30

aca aat att ggg gag gcc ctt gga cat ggc ctg gga gac gcc ctg agc 321

Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp Ala Leu Ser

35 40 45

gaa ggg gtg gga aag gcc att ggc aaa gag gcc gga ggg gca gct ggc 369

Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly Gly Ala Ala Gly

50 55 60

tct aaa gtc agt gag gcc ctt ggc caa ggg acc aga gaa gca gtt ggc 417

Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr Arg Glu Ala Val Gly

65 70 75 80

act gga gtc agg cag gtt cca ggc ttt ggc gca gca gat gct ttg ggc 465

Thr Gly Val Arg Gln Val Pro Gly Phe Gly Ala Ala Asp Ala Leu Gly

85 90 95

aac agg gtc ggg gaa gca gcc cat gct ctg gga aac act ggg cac gag 513

Asn Arg Val Gly Glu Ala Ala His Ala Leu Gly Asn Thr Gly His Glu

100 105 110

att ggc aga cag gca gaa gat gtc att cga cac gga gca gat gct gtc	561
Ile Gly Arg Gln Ala Glu Asp Val Ile Arg His Gly Ala Asp Ala Val	
115 120 125	
cgc ggc tcc tgg cag ggg gtg cct ggc cac aat ggt gct tgg gaa act	609
Arg Gly Ser Trp Gln Gly Val Pro Gly His Asn Gly Ala Trp Glu Thr	
130 135 140	
tct gga ggc cat ggc atc ttt ggc tct caa ggt ggc ctt gga ggc cag	657
Ser Gly Gly His Gly Ile Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln	
145 150 155 160	
ggc cag ggc aat cct gga ggt ctg ggg act ccg tgg gtc cac gga tac	705
Gly Gln Gly Asn Pro Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr	
165 170 175	
ccc gga aac tca gca ggc agc ttt gga atg aat cct cag gga gct ccc	753
Pro Gly Asn Ser Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro	
180 185 190	
tgg ggt caa gga ggc aat gga ggg cca cca aac ttt ggg acc aac act	801
Trp Gly Gln Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr	
195 200 205	
cag gga gct gtg gcc cag cct ggc tat ggt tca gtg aga gcc agc aac	849
Gln Gly Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn	
210 215 220	
cag aat gaa ggg tgc acg aat ccc cca cca tct ggc tca ggt gga ggc	897
Gln Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly	
225 230 235 240	
tcc agc aac tct ggg gga ggc agc ggc tca cag tcg ggc agc agt ggc	945
Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser Gly	
245 250 255	
agt ggc agc aat ggt gac aac aac aat ggc agc agc agt ggt ggc agc	993

Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly Gly Ser	
260 265 270	
agc agt ggc agc agc agt ggc ggc agc agt ggc ggc agc agt ggt ggc	1041
Ser Ser Gly Ser Ser Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly	
275 280 285	
agc agt ggc aac agt ggt ggc agc aga ggt gac agc ggc agt gag tcc	1089
Ser Ser Gly Asn Ser Gly Gly Ser Arg Gly Asp Ser Gly Ser Glu Ser	
290 295 300	
tcc tgg gga tcc agc acc ggc tcc tcc tcc ggc aac cac ggt ggg agc	1137
Ser Trp Gly Ser Ser Thr Gly Ser Ser Ser Gly Asn His Gly Gly Ser	
305 310 315 320	
ggc gga gga aat gga cat aaa ccc ggg tgt gaa aag cca ggg aat gaa	1185
Gly Gly Gly Asn Gly His Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu	
325 330 335	
gcc cgc ggg agc ggg gaa tct ggg att cag aac tct gag acg tct cct	1233
Ala Arg Gly Ser Gly Glu Ser Gly Ile Gln Asn Ser Glu Thr Ser Pro	
340 345 350	
ggg atg ttt aac ttt gac act ttc tgg aag aat ttt aaa tcc aag ctg	1281
Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser Lys Leu	
355 360 365	
ggt ttc atc aac tgg gat gcc ata aac aag aac cag gtc ccg ccc ccc	1329
Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asn Gln Val Pro Pro Pro	
370 375 380	
agc acc cga gcc ctc ctc tac ttc agc cga ctc tgg gag gat ttc aaa	1377
Ser Thr Arg Ala Leu Leu Tyr Phe Ser Arg Leu Trp Glu Asp Phe Lys	
385 390 395 400	
cag aac act cct ttc ctc aac tgg aaa gca att att gag ggt gcg gac	1425
Gln Asn Thr Pro Phe Leu Asn Trp Lys Ala Ile Ile Glu Gly Ala Asp	

405	410	415	
gcg tca tca ctg cag aaa cgt gca ggc aga gcc gat cag aac tac aat			1473
Ala Ser Ser Leu Gln Lys Arg Ala Gly Arg Ala Asp Gln Asn Tyr Asn			
420	425	430	
tac aac cag cat gcg tat ccc act gcc tat ggt ggg aag tac tca gtc			1521
Tyr Asn Gln His Ala Tyr Pro Thr Ala Tyr Gly Gly Lys Tyr Ser Val			
435	440	445	
aag acc cct gca aag ggg gga gtc tca cct tct tcc tcg gct tcc cgg			1569
Lys Thr Pro Ala Lys Gly Gly Val Ser Pro Ser Ser Ser Ala Ser Arg			
450	455	460	
gtg caa cct ggc ctg ctg cag tgg gtg aag ttt tgg tag gcaatttctt			1618
Val Gln Pro Gly Leu Leu Gln Trp Val Lys Phe Trp			
465	470	475	
gcaaccacca ccgaggcccc gaaaagcact ggtcgtcagg gagctcctcc ctttggtccc			1678
cagcctgtgc cagccctggc ccggctgcca cacctctgtt tcctaggctg gggacctcagc			1738
ttgtctctcc ttgtttcttc ccactgcact gtgggtgcttc agtggccacc agcctcgtca			1798
catacaccag catctttctg tacctcctcc ctttggtgac ctgaagtcac tgtgacagtt			1858
ctccaggaag gaggagcttc ctacttttga gtttctctgt ggaaataaaa catgaatctt			1918
gtttccctaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa			1978
aaaa			1982

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- <211> 476
- <212> PRT
- <213> Homo sapiens

<400> 8

Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys Leu
 1 5 10 15

Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser Thr Gly
 20 25 30

Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp Ala Leu Ser
 35 40 45

Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly Gly Ala Ala Gly
 50 55 60

Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr Arg Glu Ala Val Gly
 65 70 75 80

Thr Gly Val Arg Gln Val Pro Gly Phe Gly Ala Ala Asp Ala Leu Gly
 85 90 95

Asn Arg Val Gly Glu Ala Ala His Ala Leu Gly Asn Thr Gly His Glu
 100 105 110

Ile Gly Arg Gln Ala Glu Asp Val Ile Arg His Gly Ala Asp Ala Val
 115 120 125

Arg Gly Ser Trp Gln Gly Val Pro Gly His Asn Gly Ala Trp Glu Thr
 130 135 140

Ser Gly Gly His Gly Ile Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln
 145 150 155 160

Gly Gln Gly Asn Pro Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr
 165 170 175

Pro Gly Asn Ser Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro
 180 185 190

Trp Gly Gln Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr
 195 200 205

Gln Gly Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn
 210 215 220

Gln Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly
 225 230 235 240

Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser Gly
 245 250 255

Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly Gly Ser
 260 265 270

Ser Ser Gly Ser Ser Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly
 275 280 285

Ser Ser Gly Asn Ser Gly Gly Ser Arg Gly Asp Ser Gly Ser Glu Ser
 290 295 300

Ser Trp Gly Ser Ser Thr Gly Ser Ser Ser Gly Asn His Gly Gly Ser
 305 310 315 320

Gly Gly Gly Asn Gly His Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu
 325 330 335

Ala Arg Gly Ser Gly Glu Ser Gly Ile Gln Asn Ser Glu Thr Ser Pro
 340 345 350

Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser Lys Leu
 355 360 365

Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asn Gln Val Pro Pro Pro
 370 375 380

Ser Thr Arg Ala Leu Leu Tyr Phe Ser Arg Leu Trp Glu Asp Phe Lys
385 390 395 400

Gln Asn Thr Pro Phe Leu Asn Trp Lys Ala Ile Ile Glu Gly Ala Asp
405 410 415

Ala Ser Ser Leu Gln Lys Arg Ala Gly Arg Ala Asp Gln Asn Tyr Asn
420 425 430

Tyr Asn Gln His Ala Tyr Pro Thr Ala Tyr Gly Gly Lys Tyr Ser Val
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Lys Thr Pro Ala Lys Gly Gly Val Ser Pro Ser Ser Ser Ala Ser Arg
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Val Gln Pro Gly Leu Leu Gln Trp Val Lys Phe Trp
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ctgctcccag taacgtgagg

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20 25 30

Gln Lys Arg Ala Gly Gly Ala Asp Gln Phe Ser Lys Pro Glu Ala Arg
35 40 45

Gln Asp Leu Ser Ala Asp Ser Ser Lys Asn Tyr Tyr Asn Asn Gln Gln
50 55 60

Val Asn Pro Thr Tyr Asn Trp Gln Tyr Tyr Thr Lys Thr Thr Ala Lys
65 70 75 80

Ala Gly Val Thr Pro Ser Ser Ser Ser Ala Ser Arg Ala Gln Pro Gly
85 90 95

Leu Leu Lys Trp Leu Lys Phe Trp
100